

Figure 1

10 30 50  
 CGACCCACGCGTCCGCCCCACGCGTCCGGAGAACCTTTGCACGCGCACAACTACGGGGAC  
 70 90 110  
 GATTTCTGATTGATTTTTGGCGCTTTTCGATCCACCCTCCTCCCTTCTCATGGGACTTTGG  
 M G L W  
 130 150 170  
 GGACAAAGCGTCCCGACCGCCTCGAGCGCTCGAGCAGGGCGCTATCCAGGAGCCAGGACA  
 G O S V P T A S S A R A G R Y P G A R T  
 190 210 230  
 GCGTCGGGAACCAGACCATGGCTCCTGGACCCCAAGATCCTTAAGTTCGTCGTCTTCATC  
 A S G T R P W L L D P K I L K F V V F I  
 250 270 290  
 GTCGCGGTTCTGCTGCCGGTCCGGGTGACTCTGCCACCATCCCCCGGCAGGACGAAGTT  
 V A V L L P V R V D S A T I P R Q D E V  
 310 330 350  
 CCCCAGCAGACAGTGGCCCCACAGCAACAGAGGCGCAGCCTCAAGGAGGAGGAGTGTCCA  
 P Q Q T V A P Q Q Q R R S L K E E E C P  
 370 390 410  
 GCAGGATCTCATAGATCAGAATATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGAT  
 A G S H R S E Y T G A C N P C T E G V D  
 430 450 470  
 TACACCATTGCTTCCAACAATTTGCCTTCTTGCCTGCTATGTACAGTTTGTAAATCAGGT  
 Y T I A S N N L P S C L L C T V C K S G  
 490 510 530  
 CAAACAAATAAAAGTTCTGTACCAGCAGGACACCGTGTGTAGTGTGAAAAAGGA  
 Q T N K S S C T T T R D T V C Q C E K G  
 550 570 590  
 AGCTTCCAGGATAAAAACTCCCCTGAGATGTGCCGGACGTGTAGAACAGGGTGTCCCAGA  
 S F Q D K N S P E M C R T C R T G C P R  
 610 630 650  
 GGGATGGTCAAGGTCAGTAATTGTACGCCCGGAGTGACATCAAGTGCAAAAATGAATCA  
 G M V K V S N C T P R S D I K C K N E S  
 670 690 710  
 GCTGCCAGTTCCTACTGGGAAAACCCAGCAGCGGAGGAGACAGTGACCACCATCCTGGGG  
 A A S S T G K T P A A E E T V T T I L G  
 730 750 770  
 ATGCTTGCCTCTCCCTATCACTACCTTATCATCATAGTGGTTTTAGTCATCATTTTAGCT  
 M L A S P Y H Y L I I I V V L V I I L A  
 790 810 830  
 GTGGTTGTGGTGGCTTTTCATGTCGGAAGAAATTCATTTCTTACCTCAAAGGCATCTGC  
 V V V V G E S C R K K F I S Y L K G I C  
 850 870 890  
 TCAGGTGGTGGAGGAGGTCCCGAACGTGTGCACAGAGTCCTTTCCGGCGGCGTTTCATGT  
 S G G G G G P E R V H R V L F R R R S C  
 910 930 950  
 CCTTCACGAGTTCTTGGGGCGGAGGACAATGCCCGCAACGAGACCCTGAGTAACAGATAC  
 P S R V P G A E D N A R N E T L S N R Y

Figure 1 (continued)

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          970              990              1010
TTGCAGCCCACCCAGGTCTCTGAGCAGGAAATCCAAGGTCAGGAGCTGGCAGAGCTAACA
L Q P T Q V S E Q E I Q G Q E L A E L T
          1030              1050              1070
GGTGTGACTGTAGAGTCGCCAGAGGAGCCACAGCGTCTGCTGGAACAGGCAGAAGCTGAA
G V T V E S P E E P Q R L L E Q A E A E
          1090              1110              1130
GGGTGTCAGAGGAGGAGGCTGCTGGTTCCAGTGAATGACGCTGACTCCGCTGACATCAGC
G C Q R R R L L V P V N D A D S A D I S
          1150              1170              1190
ACCTTGCTGGATGCCCTCGGCAACACTGGAAGAAGGACATGCAAAGGAAACAATTCAGGAC
T L L D A S A T L E E G H A K E T I Q D
          1210              1230              1250
CAACTGGTGGGCTCCGAAAAGCTCTTTTATGAAGAAGATGAGGCAGGCTCTGCTACGTCC
Q L V G S E K L F Y E E D E A G S A T S
          1270              1290              1310
TGCCTGTGAAAGAATCTCTTCAGGAAACCAGAGCTTCCCTCATTTACCTTTTCTCCTACA
C L *
          1330              1350              1370
AAGGGAAGCAGCCTGGAAGAAACAGTCCAGTACTTGACCCATGCCCAACAACTCTACT
          1390              1410              1430
ATCCAATATGGGCGAGCTTACCAATGGTCCTTAGAACTTTGTAAACGCACTTGGAGTAATT
          1450              1470              1490
TTTATGAAATACTGCGTGTGATAAGCAAACGGGAGAAATTTATATCAGATTCTTGGCTGC
          1510              1530              1550
ATAGTTATACGATTGTGTATTAAGGGTCGTTTTAGGCCACATGCGGTGGCTCATGCCTGT
          1570              1590              1610
AATCCCAGCACTTTGATAGGCTGAGGCAGGTGGATTGCTTTGAGCTCGGGAGTTTGAGAC
          1630              1650              1670
CAGCCTCATCAACACAGTGAAACTCCATCTCAATTTAAAAAGAAAAAAGTGGTTTTAG
          1690              1710              1730
GATGTCATTCTTTGCAGTTCTTCATCATGAGACAAGTCTTTTTTCTGCTTCTTATATTG
          1750              1770              1790
CAAGCTCCATCTCTACTGGTGTGTGCATTTAATGACATCTAACTACAGATGCCGCACAGC
          1810              1830              1850
CACAATGCTTTGCCTTATAGTTTTTTAACTTTAGAACGGGATTATCTTGTTATTACCTGT
          1870              1890              1910
ATTTTCAGTTTCGGATATTTTTGACTTAATGATGAGATTATCAAGACGTAGCCCTATGCT
          1930              1950              1970
AAGTCATGAGCATATGGACTTACGAGGGTTCGACTTAGAGTTTTGAGCTTTAAGATAGGA
          1990              2010              2030
TTATTGGGGCTTACCCACCTTAATTAGAGAAACATTTATATTGCTTACTACTGTAGGC
          2050              2070              2090
TGTACATCTCTTTTCCGATTTTTGTATAATGATGTAAACATGGAAAACTTTAGGAAATG
          2110              2130              2150
CACTTATTAGGCTGTTTACATGGGTGCTTGATACAAATCAGCAGTCAAAAATGACTAA
          2170              2190              2210
AAATATACTAGTGACGGAGGGAGAAATCCTCCCTCTGTGGGAGGCACTTACTGCATTCC

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Figure 1 (continued)

2230	2250	2270
AGTTCTCCCTCCTGCGCCCTGAGACTGGACCAGGGTTTGATGGCTGGCAGCTTCTCAAGG		
2290	2310	2330
GGCAGCTTGCTTACTTGTTAATTTTAGAGGTATATAGCCATATTTATTTATAAATAAAT		
2350	2370	2390
ATTTATTTATTTATTTATAAGTAGATGTTTACATATGCCCAGGATTTTGAAGAGCCTGGT		
2410	2430	2450
ATCTTTGGGAAGCCATGTGTCTGGTTTGTCTGCTGGGACAGTCATGGGACTGCATCTTC		
2470	2490	2510
CGACTTGTCACAGCAGATGAGGACAGTGAGAATTAAGTTAGATCCGAGACTGCGAAGAG		
2530	2550	2570
CTTCTCTTTCAAGCGCCATTACAGTTGAACGTTAGTGAATCTTGAGCCTCATTTGGGCTC		
2590	2610	2630
AGGGCAGAGCAGGTGTTTATCTGCCCCGGCATCTGCCATGGCATCAAGAGGGAAGAGTGG		
2650	2670	2690
ACGGTGCTTGGAATGGTGTGAAATGGTTGCCGACTCAGGCATGGATGGGCCCCCTCTCGC		
2710	2730	2750
TTCTGGTGGTCTGTGAACTGAGTCCCTGGGATGCCTTTTAGGGCAGAGATTCCTGAGCTG		
2770	2790	2810
CGTTTTAGGGTACAGATTCCTGTGAGGAGCTTGGCCCCCTCTGTAAGCATCTGACTCA		
2830	2850	2870
TCTCAGAGATATCAATTCTTAACACTGTGACAACGGGATCTAAAATGGCTGACACATTT		
2890	2910	2930
GTCCTTGTCACGTTCCATTATTTTATTTAAAAACCTCAGTAATCGTTTTAGCTTCTTT		
2950	2970	2990
CCAGCAAACCTCTCTCCACAGTAGCCAGTCGTGGTAGGATAAATTACGGATATAGTCAT		
3010	3030	3050
TCTAGGGGTTTCAGTCTTTTCCATCTCAAGGCATTGTGTGTTTGTTCGGGACTGGTTT		
3070	3090	3110
GGCTGGGACAAAGTTAGAACTGCCTGAAGTTCGCACATTCAGATTGTTGTGTCCATGGAG		
3130	3150	3170
TTTTAGGAGGGGATGGCCTTTCCGGTCTTCGCACTTCCATCCTCTCCCCACTTCCCATCT		
3190	3210	3230
GGCGTCCCACACCTTGTCCCCCTGCACCTTCTGGATGACCAGGGTGCTGCTGCCTCCTAGT		
3250	3270	3290
CTTTGCCTTTGCTGGGCCCTTCTGTGCAGGAGACTTGGTCTCAAAGCTCAGAGAGAGCCAG		
3310	3330	3350
TCCGGTCCCAGCTCCTTTGTCCCTTCCCTCAGAGGCCCTTCCTTGAAGATGCATCTAGACTA		
3370	3390	3410
CCAGCCTTATCAGTGTTAAGCTTATTCCTTTAACATAAGCTTCCTGACAACATGAAATT		
3430	3450	3470
GTTGGGGTTTTTTGGCGTTTGTGATTGTTTAGGTTTTGCTTTATACCCGGGCCAAATA		
3490	3510	3530
GCACATAACACCTGGTTATATATGAAATACTCATATGTTTATGACCAAAATAAATATGAA		
3550		
ACCTCAAAAAAAAAAAAAAAAAAAAAA		

## Figure 2

**L** L I W - - - L P M V S A R S K S V H Q V T D I N S K - L E R K T V T T V E T Q N L - E G L Q F P C h Pas  
1 N G A - - - A T R A N D P R U L L L L V L C - - - A B E C T G I Y T S G E C C K A s h NGFR p75  
1 - L S V P D L L P L L L L - V I Y P S V I G V P H - D R E K D S V C P Q E Y I - H - P A N N S I Q T S t h TNFR 1  
1 - L U G O - - - V D T A - - - S S A R A TRIO  
1 A P P P A R V H L G A P A V P N P S A A S G T E A A A T P S K V G S A A I E P R G R G L D T S H G N L P S A R A S A CR-4

64 P P R K R R D T V D B P C V P Q E K E Y D K A N P S S K R R C R L D E G H L E E E N - - - - - C R h Pas  
48 N L S V V Q F E Q T V C E - - - D S T S - D V S A T E P C P C - - - E C V L L S - - - M S A P V Z h NGFR p75  
63 H K T Y L Y N D P G P Q D T C R E S S G F A S E N H L R H L C S A K K E M P - C E S S - - - C V z h TNFR 1  
17 S R Y P A R T S S T R P W L - - - I P G I A A L P R V D S T I P Q D B V P Q T V A P V Q R R S L K E E P A T P IO  
71 S E A P P R P R E T S P R R V - H T P P W - - - G L L Q V P S A A I K - - - L H D Q S T J C W H S P L G E L P CR-4

122 T Q N - - - T K - - - K P N - - - F P N - - - S V N - - - - - - - R H - - - h Pas  
102 A D - - - A V - - - A Y I Y - - - Q D E T T G - R E A R C B A S G L V P S Q D K H T V E E P D O T Y S R E A N H v h NGFR p75  
120 D R - - - T V - - - G R K N - - - R H Y W E L F Q P N S L L N - - - V H L S C Q E K E R V G T - H A M P L R E E z h TNFR 1  
96 S H R S B Y T S A N P R E S D I X - - - S N L P S L L V C R E Q N K S S C T T R D V C - - - R H S : Q L K H S P - TRIO  
135 S H R S B R P R A N S T E R Q V N - - - E N L E A - P T A K E D E E R P C T T R E A A - - - K P S T E R N D H S A - CR-4

143 - - - D E T K - - - H I - - - I E - - - L T S T C K E G S R W - - - - - H I C A N - L D h Pas  
162 D P L E C - V E O T E R Q L R E C R A A E E E I P G R W I R S P P E S D S A P T O E E A P E Q D L A S T A G h NGFR p75  
159 - - - V S - - - N - - - K S L E C T L - - - - - - - L P Q I E V K R T D S G T V L D I V I P F R - U C L S L f h TNFR 1  
171 E C C T R G P G A V A S N R - - - K K N E S A A S S G P - A A E V T E G M L A S S Y H Y I I V V L V TRIO  
202 E C C K S T P P G A V A S D - - - E E S E V H - - - E S - - - N G H N I W - - - - - V V T L S V E CR-4

184 P I I - - - - - V W K R E Q K T H H R K I N Q I H S P I - - - N - - - - - - - - - - - - - V A I - N L C B D L S K Y i t h Pas  
231 V V T T M G S S - - - Q P - - - T R G T T D N L F V Y C S L A A V V V - - - A Y A I A K E W N S K Q N K Q C H N S R P V C O P P h NGFR p75  
230 G M Y R Y Q R W - K S P L Y S I V G S T P K E E L G T T K P A - - - N P S S P T P L P S P P S S T F T S h TNFR 1  
221 I A A - - - - - G P S - - - K F I S Y L K G C S G G H P B R H V L R R - - - S P S V P G E B U N R E L S TRIO  
252 L L V A - - - - - L I V C C - - - - - G S C C G P K C M D C C W L - - - L L G R E E N H M T C CR-4

235 T - - - - - I G V M T L S Q V - - - - - L P A K R E E V E K L - - - - - h Pas  
296 P E G K L H S D G I S V D S H H Q Q P H Q T A S Q R - - - K G G L Y S - - - - - L P A K R E E V E K L - - - - - h NGFR p75  
296 S T Y T G D C P N P A A P R R V - - - P P Y O G A D L T A A S P I P N P L K W E D S A H K P Q S L D I D P A T L Y A V V h TNFR 1  
282 R Y L Q G O S E R I Q Q E A R R G V V R E B P R L E Q A E A E C Q R R R L V P V D E S A - - - - - TRIO  
302 A D S L S P F E Q H E C R P P P V T Q R E A C E L P A R A E S S S P L L V P A G E P E T M L P P D K F CR-4

245 - - - - - G P F K N V N E A K - - - R I K N D V Q D T A Q K V Q E R N H Q L H K K E - Y D - I K D K K A N C T h Pas  
352 - - - G S A G D T R H A G E Y Q P E H S P T - H E A C - - - P V R R L L S A T Q D S - - - A T A A I A A R E I Q R A D h NGFR p75  
164 E V P L - R E F - - - R S D H - - - R L E L Q G R C L R - - - Q S M - T M R R R - - - P R E C E L G R V - D D L G h TNFR 1  
343 - - - - - I S L L D A S A T L S E G - - - - - TRIO  
372 A I V P D S D Q Q M Q D T K N E - - - V V R - A G T A G P G D L V M H K K V N K E E N - N I K P L L D A P H H E R CR-4

306 L A T T T I L K D I T S D S N N P R N E I Q S V h Pas  
413 - - - - - E - - - - - L C S - - - T T P - - - h NGFR p75  
433 C L E D E A A - - - - - C G P A A L P P P L R h TNFR 1  
358 K K T T Q Q L G E R L F R D E G A T C R  
440 A K S K I L L D G E F I L E D G T S A V E - E TRIO  
  
TR-4

Decoration 'Decoration 11': Shade (with solid black) residues that match the Consensus exactly.

Figure 3

